



Genetic Stocks-Oryza (GSOR) Collection

2013 Update



Rice Genetic Stocks Collection

The USDA Genetic Stocks – *Oryza* (GSOR) Collection at DBNRRC serves as distribution center for genetic mutants and molecularly characterized genetic resources that are important to the rice research community. These genetic stocks have been created using specialized techniques such as induced mutation and cross-breeding. The GSOR program is responsible for storing, maintaining, documenting, and distributing (free of charge) these materials to the scientific community for use in genetic and genomic research. Ultimately these materials will aid in the understanding of the genetic control of traits that can be used to enhance the development of new cultivars that meet the needs of the U.S. rice industry.

Growth of GSOR Collection

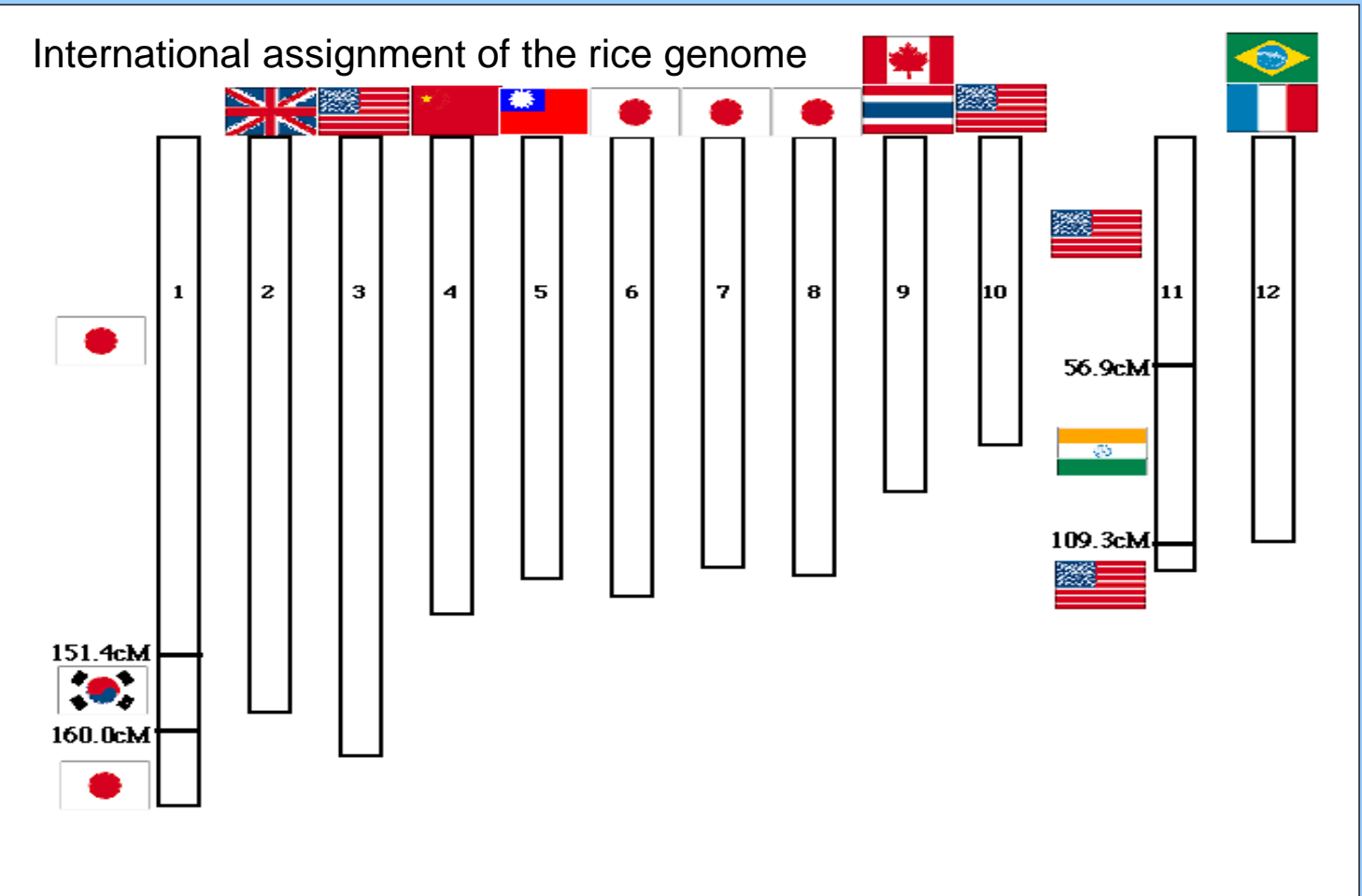
Year Rec'd	TYPE OF ENTRY	ENTRIES
2003-4	Individual mutants	20
2005	K/Z Mapping population	355
	Nipponbare	1
2006	Cocodrie/McR01 Mapping population	327
	Individual mutants	8
	Kinoshita Mutant Collection	192
2007	Jodon Mutant Collection	38
	California Mutant Collection	12
	Early/Katy Mapping population	240
	USDA Core Collection	1794
2008	Katy Deletion (Putative) Mutants	22842
	Nipponbare TILLING Mutants	6397
2009	Cybonnet x C101A51 Mapping population*	183
	RiceCAP Association Mapping population*	462
	RiceCAP MY1 Mapping population	219
	RiceCAP MY2 Mapping population	300
	RiceCAP SB5 Mapping population	574
2010	OryzaSNP Set	20
2011	TeQing-into-Lemont (TILs) mapping population	125
	NSF Rice Diversity Panel	404
2012	BC5F3 Backcrossing Population	44
2013	Rice Diversity Panel 2*	1333

*Not yet publicly available. Grand Total Lines 35890

Mapping populations are used to study the genetic variation which occurs as a result of recombination of genes from two differing parental lines. The mapping populations in the collection are segregating for agronomic traits, disease resistance, maturity, yield, milling quality, and cooking quality.

TILLING (Targeting Induced Local Lesions In Genomes) is a reverse genetics technique that uses traditional chemical mutagenesis to create libraries of individual rice plants can be evaluated using high throughput screens for the discovery of mutations. (Source: http://tilling.ucdavis.edu/index.php/Main_Page)

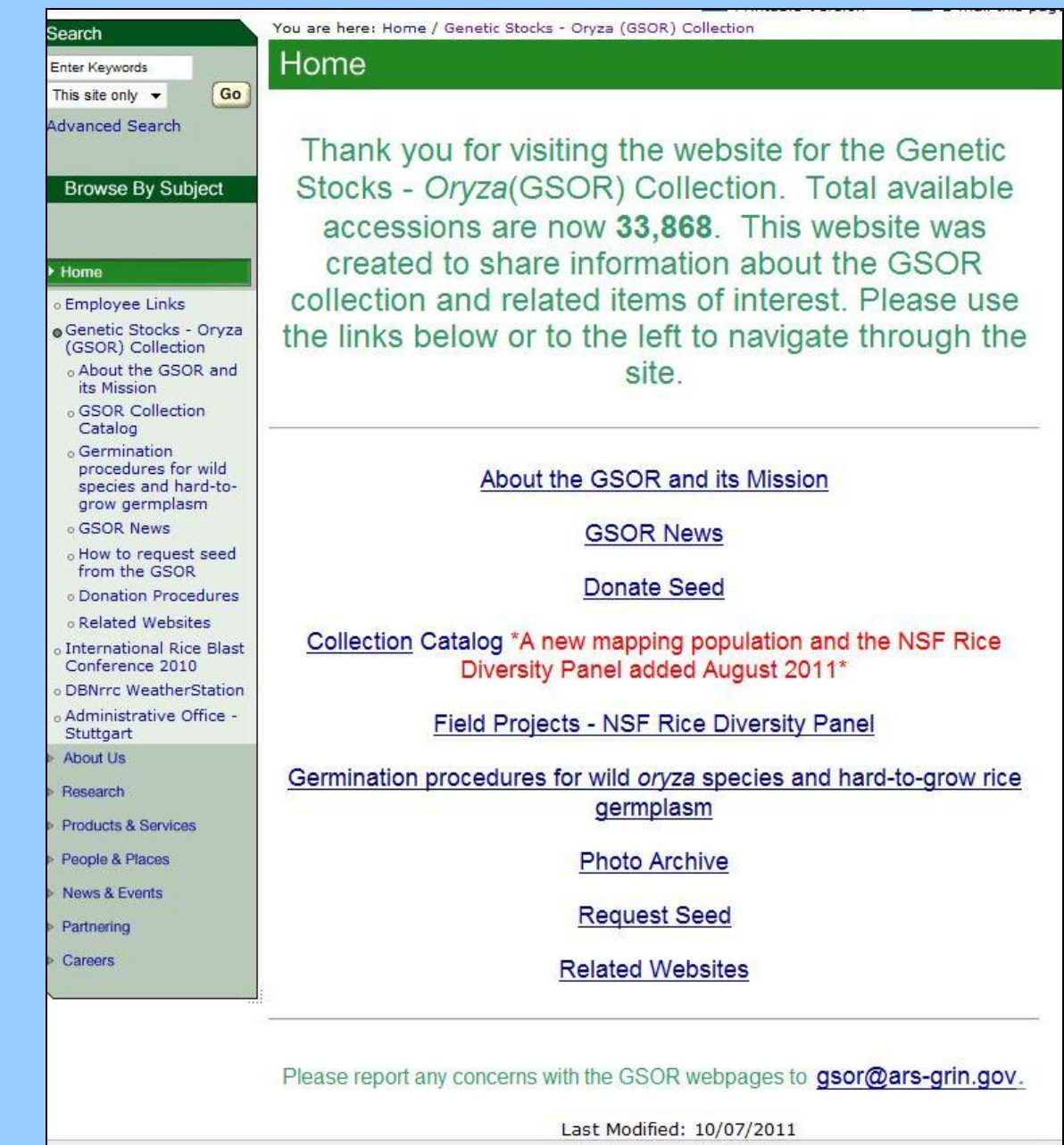
The graphic at the right shows the assignment of the 12 chromosomes of rice to 10 different nations that participated in the International Rice Genome Sequencing Project. In 2005, this international consortium produced the complete genetic sequence of the Japanese cultivar, **Nipponbare**. This sequence information will serve as the baseline for comparison with other rice varieties to identify genes that control economically important traits. GSOR serves as an international distributor of the exact source of Nipponbare that was sequenced for use in genomic research.



Distribution Activity to U.S. and International Researchers

32,586 genetic stocks were distributed during the years 2004 through 2012 (combined). During 2013 there have been 2,802 genetic stocks distributed as of February 4.

Data Collection - Barcoding software and handheld data collection devices are used to streamline data collection, inventory, and distribution activities.



Website: www.ars.usda.gov/spa/dbnrrc/gsor
Resources available on the website include a collection catalog, photos from current field projects and germination procedures for hard-to-grow rice germplasm.

New inventory codes have been created to indicate source of GSOR seeds. The six-digit code shows the location, year, season, and purity of seed. 1 2 3 4 5 6: 1 = location (A-Arkansas, T-Texas, P-Puerto Rico, G-Greenhouse in Arkansas), 2-3= Year (last 2 digits of production year(s), 4-5 = Season (Fall, Spring, Summer, Winter), and 6=Purity (1=panicle, 2=plant, 3=bulk). Example: A11FA3 = Arkansas, 2011, Fall, Bulk harvest.

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